

EXHIBIT 10

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap and extension gap penalties
gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSUVALSLIDUYGNSFYESTULTHALSSQFMLSISEASUNQLRSUUFSGULNVFHYGWUJ  
LWTWGWAKTQDEPASPATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHFPWGITGGGLGMMVYQDFRENHPGFHMRSSGYSAGMIAGQHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSQCGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFY  
QGENLTSQGTFRSQTMGGAFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMMATQRPQAWTVELAYQFVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGETALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
ITLNAVNLVDALGNAYEDFILATSRFFTAIVATINASTVIQFTUNLTNYVFFTHYUQJN  
WTVIWDDETATKTATLIWEQTGYSPNERQGPLVPNTLWGAFSDLRAIQNLMDISVNGAD  
YHRGFVWSGLANFLHKSGSDTKRKFRHNSAGYALGVYAKTPSDDIFSAAFQQLFGKDKDY  
LVSKNNANIYAGSLYYQHSIYWSAWQNLQNTIGAEAPLVLNAQLTYCHASNDMKTMTT  
TYAPRKTTYAEIKGDWGNDCFGVELGATVPIQTESLLFDMYSPFLKFQLVHTHQDDFKE  
NNSDQGRYFESSNLTNLSLPIGKFERFANNDTASYHVTAAYSPDIVRSNPDCSTSLVS  
PDSAVVVTKANLARSFMLQAGNYLSLSHNIEIFSQFGFELRGSSRTYNVDLGSKIQF
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



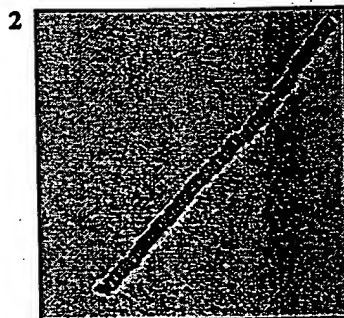
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lc|seq_1 Length 965 (1..965)

Sequence 2 lc|seq_2 Length 839 (1..839)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 153 bits (386), Expect = 2e-35

Identities = 201/781 (25%), Positives = 320/781 (40%), Gaps = 114/781 (14%)

```
Query: 189 TFVSENQSCFLFMDNICIQNTAGKGGAIYA-GTSNSFESNNCDLFFINNACCAGGAIF 247
      TF+ + CF DNI T TA GAI G + + LF + A C G
Sbjct: 85 TFLGNGYTLCF---DNI---TTTASNPGAINVQGGKTLGISGSLF--SCAYCPPGTTG 136

Query: 248 SPICSLTGN-----RGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVD---GNRGRI 299
      GN ++VF+ KN TA +GGAI+ D N +
Sbjct: 137 YGAIQTKGNTTLKDNSSLVFH-----KNCSTA-----EGGAIQCKGSSDAELKIENNQNL 186

Query: 300 FFSDNITKNYGGAIYAPVVTLDVNGPTYFXXXXXXXXXX-----XXKDGTNSNKISADR 354
      PS+N + + GGAIYA +T+V GPT F D + , ++AD
Sbjct: 187 VFSSENSSTSKGGAIYADKLTIIVSGGPTLFSNNSVSNSSPKGGAISIKDSSGECSLTADL 246

Query: 355 HAIIFNENIVTNVNTNANGTSTSANPRRNAITVASSSGEILLGAGSSQNLIIFYDPIEVSN 414
      I F+ N + + + T T RN+I + + L A + FYDPI
Sbjct: 247 GDITFDGNKIIRKSGSSSTVT-----RNSIDLGTGKFT-KLRAKDGFGIFFYDPIITGGG 299

Query: 415 AG-VVSFNKEADQTSVVFSGATVNSAD-FHQRNLQTKTPAPLTLNGLFCIEDHAQLT 472
      + ++++ + D TG +VFSG ++ + NL + P+TSL G L ++D +T
Sbjct: 300 SDELNINKKETVDYTGKIVFSGEKLSDDEEKARAENLASTFNQPIITLSAGSLVLKDGVSVT 359

Query: 473 VNRFTQ-TGGVVSILGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLV 531
      + TQ G V + G L +G +ITL ++ +N++S+ G
Sbjct: 360 AQTQTEAGSTVMDLGTTLQTPSSGG-----ETITLTNLDINIASLGGGG-----T 407

Query: 532 EPTNNSNNYTADTAATFSLSDVKLSLIDYGNSPYESTDLTHALSSQPMLSISEASDNQL 591
      P + N TA A T + ++L+D GN+ YE L +S+P +I ++
Sbjct: 408 SPAKLATN-TASQAITINA---VNLVDADGNA-YEDPILA---TSKPFTAIVATTNAST 458

Query: 592 RSDDMDPFGSLNVP--HYGWQGLWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLP 649
      + D VP HYG+QG WT W D E A+ +T LTW
Sbjct: 459 VTQPTDNLNYPVPPHYGYQGNWVTW---DTETAT-----KTATLTWEQ 500

Query: 650 AGYVPSPKHRSPLIANTLWG--NMLLATESLKNSAELTPSDHFFWGITGGGLGMVYQDP 707
      GY P+P+ + PL+ NTLWG + L A ++L + + H G GL +++
Sbjct: 501 TGYSFNPERRQGFLVNTLWGAFLDLRAIQNLMDISVNGADYHR--GFWVSGLANFLHKSG 558

Query: 708 RENHPGPHMRSSGYSAGMIA--GQTHTFSLKFSQTYTKLNE-RYAKN--NVSSKNYSCQG 762
```

+ F S+GY+ G+ A FS F Q + K + +KN N+ + + Q
 Sbjct: 559 SDTKRKFRHNSAGYALGVYAKTPSDDIFSAAFQQLFGKDKDYLVSKNNANIYAGSLYYQH 618
 Query: 763 EMLFSLQEGFLLTKLVGLYSYGDHN-----CHHFTYQGENLTS-----QGTFR 805
 +S + LL +G + N CH N+T+ +G +
 Sbjct: 619 ISYWSAWQN-LLQNTIGAEAPLVNAQLTYCHASNDMKTNTTTTYPRTTTYAEIKGDWG 677
 Query: 806 SQTMGGAVFFDLPMKPPGSTHI-LTAPFLGALGIYSSLSHFTVEVGAYPRSPSTKTPLINV 864
 + G + +P++ S + +PFL +++ F E + + L N+
 Sbjct: 678 NDCFGVELGATVPIQTESLLFDMYSPFLKFQLVHTHQDDFKENNSDQGRYPSSNL/TNL 737
 Query: 865 LVPIGVKGSMNATORPQAWTVELAYQFVLYRQEPGIATQLLAS--KGIWFGSGSPSSRH 922
 +PIG+K A ++ V AY P + R P T LL S +W + +R
 Sbjct: 738 SLPIGKPERF-ANNDTASYHVTAAAYSPDIVRSNPDCTTSLLVSPDSAVWVTKANNLARS 796
 Query: 923 A 923
 A
 Sbjct: 797 A 797

CPU time: 0.21 user secs. 0.04 sys. secs 0.25 total secs.

Lambda K H
 0.317 0.133 0.397

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 9430

Number of Sequences: 0

Number of extensions: 782

Number of successful extensions: 11

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 965

length of database: 326,943,915

effective HSP length: 134

effective length of query: 831

effective length of database: 281,544,581

effective search space: 233963546811

effective search space used: 233963546811

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☒ Use MegaBLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSIDVRLSLIDUYNSTFESTULITALSSQFMLSISEASINQLKSDUDDFSGLNVPHYGWUJ  
LWTWGWAKTQDFEPASSATTIDPQKANRFHRTLTLTWLPAGYVSPKHSPLIANTLWGNM  
LLATESLKNSELTTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTTLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYSKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGELALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
HYGTQSNWVIVWAQSSAQERTATLTIWEQIGTSPNFERQSLVFNLTWGSFSDIKAIQNL  
MDISVNGADYHRGFWSGLGNFLHKSGSDTKRKFRHNSAGYALGVYAQTPEDEVFSAAPC  
QLFGKDKDYLVSKNSSTVYAGSIYYQHSYWNWNTLLQNTLGAEAPLVNAQLAYCHAS  
NNMKTMTDTYAPFKITYSEIKGDWGNDCFGVEFGAKAPIETASLLPDMYSPFVKLQLVH  
AHQDDFKENNSDQGRYPESNNLTNLSMPIGVKLEKPSHKDTASYNLTLAYAPDIVRSNPD  
CTASLLVSPTSAAVWVTKANNLARHAFILQAGNYLALTRNTELFSSQFGFELRGSCRTYNID  
LGSKIQF
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



NCBI

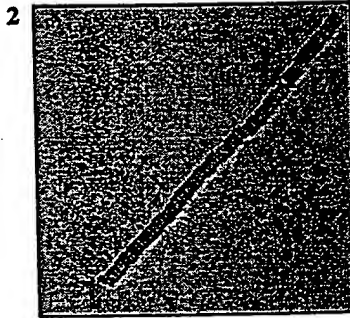
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Alien**

Sequence 1 lc|seq_1 Length 965 (1..965)

Sequence 2 lc|seq_2 Length 847 (1..847)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 165 bits (417), Expect = 4e-39
Identities = 189/767 (24%), Positives = 308/767 (39%), Gaps = 101/767 (13%)

Query: 200 LFMNLCIQNTAGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGN--- 256
L DNI T++ G +GT+ ++ + LF + A C GA GN
Sbjct: 97 LCFDNIT--TQSSHPGAISVSGTNKTLDISGFSLF--SCAYCPPGATGYGAIKAVGNTTI 152

Query: 257 --RGNIVFYNNRCFKNVETASSEADGGAIKVTTRLDVTGNRGRIFFSDNITKNYGGAIY 314
++VF+ KN T A A L + N+ +F ++N + + GGAIY
Sbjct: 153 KDNSSLVFH----KNCSTGEGGAIQCKASSSEAEKLIENNQLVFAENSSSSSGGAIY 206

Query: 315 APVVTLDVNGPTYFXXXXXXXXXXXXXX---DGTNSKISADRHAIIFNENIVTNVINA 370
A +T+V GPT F D ++AD I F+ N +
Sbjct: 207 ADKLTIVSGGPTLFSNNSVSASSPKGAICIKDSGGECSLTADLGDTITFDGNKIITNGG 266

Query: 371 NGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGVSVSFNKE--ADQT 428
+ T T RN+I + SS L A + FYDPI ++ NK+ D T
Sbjct: 267 SPTVT-----RNSIDLSSGKFTKLNAKEGFGIFFYDPI-TGGGSDELNINKQDVTVDYT 319

Query: 429 GSVVFSGATVNSADFH-QRNLQTKTPAPLTLNGLFCIEDHAQLTVNRFTQT-GGVVSLG 486
G +VPSG ++ + NL++ PL + +G L ++D L FTQT G V +
Sbjct: 320 GKIVFSGERLSDEEKVAANLKSDFKQPLKIGSGSLILKDGVTLETQSFTQTGEGATVVM 379

Query: 487 NGAVLSCYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLWVEPTNNSNNTADTAA 546
G L +G +ITL ++ +N++S+ G VE T S T +
Sbjct: 380 LGTTLQTPSSGG-----ETITLTNLDINVASLGGGVAPDPKVEATTESKTVTINA-- 431

Query: 547 TFSLSDVKLSLIDYGNSPYESTDLTHALSSQPMLSIS--EASDNQLRSDMDPFGSLNVP 604
++L+DD GN+ YE L +SQP +I S + + P
Sbjct: 432 -----VNLVDDNGNA-YEYPILA---ASQPFTAIEVRSGSSGSITKPTTNLENTFP 479

Query: 605 -HYGWQLWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLI 663
HYG+QG WT W + SSA +T LTW GY P+P+ + L+
Sbjct: 480 THYGYQGNWTVTWKQ-----GSSAQ-----EKTATLTWEQTGYSPNPERQGS 523

Query: 664 ANTLWGNMLLATESLKNSAELTPSDHPFW-GITGGGLGMMVYQDPRENHPGFHMRSSGYS 722
NTLWG+ +++N +++ + + G GLG +++ + F S+GY+
Sbjct: 524 PNTLWGS-PSDIRAIQNLMDISVNGADYHRGFWVSGLGNPLHKSGSDTKRKFHNSAGYA 582

Query: 723 AGMIA--GQTHFTSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLF-----SLQE 770

G+ A FS F Q + K ++ Y + SS Y+ G + + +L +
Sbjct: 583 LGVYAQTPESEVFSAAFCQLFGK-DKDYLVSKNSSTVYA--GSIYYQHISYWNTWNTLLQ 639
Query: 771 GFLLTKLVLGLYSYGDHNCCHFYTOGENLTS-----QGTFRSQTMGGAVFFDLP 818
L + + + CH N+T +G + + G P
Sbjct: 640 NTLGAEAPLVLAQLAYCHASNMMKTNMTDTYAPPKTTYSEIKGDWGNDCFGVEFGAKAP 699
Query: 819 MKPFGSTHILTAPFLGALGIYSSLSHPTVEVGAYPRSPSTKTPLINVLVPIGVKGSFMMAT 878
++ + +PF+ +++ F E + + L N+ +PIGVK +
Sbjct: 700 IETASLLPDMYSPFVKLQLVHAHQDDFKENNSDQGRYFESNNLTNLSMPIGVKLEKF-SH 758
Query: 879 QRPQAWTVELAYQFVLYRQEPGIATOLLAS--KGIWFGSGSPSSRHA 923
+ + + LAY P + R P LL S +W + +RHA
Sbjct: 759 KDTASYNLTLAYAPDIVRSNPDCTASLLVSPTSAPVWVTKANNLARHA 805

CPU time: 0.22 user secs. 0.03 sys. secs 0.25 total secs.

Lambda K H
0.317 0.133 0.397

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 9976

Number of Sequences: 0

Number of extensions: 824

Number of successful extensions: 14

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 965

length of database: 326,943,915

effective HSP length: 134

effective length of query: 831

effective length of database: 281,544,581

effective search space: 233963546811

effective search space used: 233963546811

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 78 (34.7 bits)

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#).
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSIVVLSLIDUIGNSPIESTULTHALSSQFRLSISEASLNQKRSULMDFSGLNVFHYGWQJ  
LWTGWAKTQDEPASPATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTKLNERVAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFT  
QGENLTSQGTFRSQTMGAVFFDLPMKPPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINLVPIGVKGSFMNATQRPQAWTVELAYQFVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGETALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
DLISVNGAUISRGFWVSSLANFLNAGSUTAKKFKHNSAGIALGVIAQTFSDDVCSAFCQ  
LFGKDKDYFVSKNSSTIYAGSIYYQHSYWNWTNTLLQNTLGAEAPLVLNAQLTYCHASN  
NMKTNMTNTYTPKNVTPSEIKGDWGNDCFGVEFGAKAPIETASLLFDMYSPFVKLQLVHA  
HQDDFKENNSDQGRYFESNNLTNLSMPIGVKLEKFSHKDTASYNLTAYAPDIVRSNPD  
TASLLVSPTSAVVWTKANNLARHAFILQAGNYLALTRNTELSQFGFELRGSCRTYNIDL  
GSKIQF
```

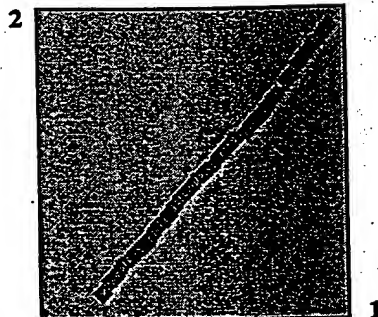
Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequ nces results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter: ☒ **Alien**

Sequence 1 **lcl|seq_1** Length 965 (1..965)Sequence 2 **lcl|seq_2** Length 846 (1..846)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 151 bits (382), Expect = 5e-35
Identities = 184/790 (23%), Positives = 312/790 (39%), Gaps = 101/790 (12%)

```
Query: 182 GAISTANTFVSENGSCFLFMDN---IC---IQNTNAGKGGAIYAGTSNSFESNNCDLFF 235
      G S N SE F+ N +C I T ++ G +GT+ + + + LF
Sbjct: 68 GKDSPLNKSCFSETTENLSFIGNGYTLCPDNITTQSSHPGAISVSGTNKTLDISGFSLFS 127

Query: 236 INNACCAG---GAIFSPICSLTGNRGNIVFYNNRCFKNVETASSEASDGGAIKVITRLD 291
      C G GAI + + + ++VF+ KN TA A + T L
Sbjct: 128 CAYCCPPGTTGYGAIQTKGTTTLKDNSSLVFH-----KNCSTAEGGAIQCKSSSSTAELK 182

Query: 292 VTGNRGRIFSDNITKNGYGAIPVVTLDVNGPTYFXXXXXXXXXXXXX-----DGTS 346
      + N+ +F S+N +K GGAIYA +T+V GPT F D
Sbjct: 183 LENNKNLVLF-SENSSKEKGGAIYADKLTIVSGGPTLFSNNSVSHNSSPKGGAICIKDSGD 241

Query: 347 NSKISADRHAIIFNENIVTNVNTANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIF 406
      ++A+ I F+ N + + T T RN+I + S L A + F
Sbjct: 242 ECLSLTANLGDITFDGNKIITNGGSPVT-----RNSIDLGGGKFTKLNAKEGFGIFF 295

Query: 407 YDPIEVSNAGVSVSFNK---EADQTSVVFSGATVNSADFH-QRNLQTKTPAPLTLNNGF 462
      YDPI + + NK + TG +VFSG ++ + NL++ PL + G
Sbjct: 296 YDPIANTGGSTEIELNKTESDITYTGKIVFSGEKLSDEEKTVPANLKSIFYKQPLKIGAGS 355

Query: 463 LCIEDHAQLTVNRFTQT-GGVVSLGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSILK 521
      L ++D L + TOT G V + G L S+S +ITL ++ +N++S+
Sbjct: 356 LVLKDGVTLEAKKITQTKGSTVVMDLGTTLQT-----PSSSGETITLTNLDINIASLGG 409

Query: 522 SGAEIFLLWVEPTNNSNNYTDATATFSLSDVKLSLIDYGNSPYESTDLTHALSSQPM 581
      G P A A+ ++S ++L++ N+ YE L+ + S +
Sbjct: 410 GGGTAPAK-----LATNTASQAISIAAVNLVNTDSNT-YEDPILSASKSFSAIT 457

Query: 582 SISEASDNQLRSDMDFSGLNVP-HYGWQGLWTGWAKTQDPEPASSATITDPQKANRFH 640
      ++ +S + + + P HYG+QG WT W + SSA
Sbjct: 458 ATTSSST--VTPPETNLKNYTPPTHYGYQGNWTVTWKQ-----GSSAQ-----E 499

Query: 641 RTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHPF-WGITGGGL 699
      +T LTW GY P+P+ L+ NTLWG T +++N +++ + G L
Sbjct: 500 KTATLTWEGTGYSPNPERVGSGLVPNTLWG-AFSDTRAQNLMDISVNGADYSRGFWVSSL 558
```

Query: 700 GMMVYQDPRENHPGFHMRSSGYSAGMIA--GQTHTFSLKFSQTYTKLNERYAKNNVSSKN 757
++ + F S+GY+ G+ A S F Q+ K++ N SS
Sbjct: 559 ANFLNKSQSDTKRKFRHHSAGYALGVYAQTPSDDVCSAAFCQLFGKDKDYFVSKN-SSTI 617

Query: 758 YSCQGEMLP-----SLQEGFLITKLVLGLYSYGDHNCCHFYTQGENLTS----- 800
Y+ G+ + +L+ L+ + + CH N+T+
Sbjct: 618 YA--GSIYYQHISYWNWNTLLQNTLGAEAPLVLNAQLTYCHASNMMKTNTNTYTPKNV 675

Query: 801 -----QGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHPTVGVAYPRSP 855
+G+ + G P++ + +PF+ +++ FE + +
Sbjct: 676 TPSEIRGDWGNDCFGVEFGAKAPIETASLLFDMYSPFVKLQLVHAHQDDFKENNSDQGRY 735

Query: 856 STKTPLINVLVPIGVKGSEFMNATQRPQAWTVELAYQFVLYRQEPGIATQLLAS--KGIWF 913
L N+ +PIGVK + + ++ + LAY P+ R P LL S +W
Sbjct: 736 FESNNLTNLSMPIGVKLEKF-SHKDTASYNLTLAYAPDIVRSNPDCTASLLVSPTS AVVW 794

Query: 914 GSGSPSSRHA 923
+ +RHA
Sbjct: 795 TKANNLARHA 804

CPU time: 0.25 user secs. 0.03 sys. secs 0.28 total secs.

Lambda K H
0.317 0.133 0.397

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 9987

Number of Sequences: 0

Number of extensions: 805

Number of successful extensions: 11

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 965

length of database: 326,943,915

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A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

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S1: 41 (21.6 bits)

S2: 78 (34.7 bits)